

FIGURE 1

TAQ DNA POLYMERASE SEQUENCE
1/6

-120 -100 -80
BglII *PvuII*

AAGCTCAGATCTACCTGCCTGAGGGCGTCGGTTCAAGCTGCCCTTCCCGAGGGGAGA

-60 -40 -20

GGGAGGCCTTCTAAAGCCCTTCAGGACGCTACCCGGGGCGGTGGTGGAAAGGTAAC

1 20 40 60

ATGAGGGGGATGCTGCCCTCTTGAGCCAAGGGCCGGTCCCTGGTGGACGGCAC

MetArgGlyMetLeuProLeuPheGluProLysGlyArgValLeuLeuValAspGlyHis

1

80 100 120

CACCTGGCCTACCGCACCTCCACGCCCTGAAGGGCCTCACCAACCAGCCGGGGAGCCG

HisLeuAlaTyrArgThrPheHisAlaLeuLysGlyLeuThrThrSerArgGlyGluPro

140 160 180

GTGCAGGCGGTCTACGGCTCGCCAAGAGCCTCCTCAAGGCCCTCAAGGAGGACGGGAC

ValGlnAlaValTyrGlyPheAlaLysSerLeuLeuLysAlaLeuLysGluAspGlyAsp

41

200 220 240

GCGGTGATCGGGTCTTGACGCCAAGGCCCTCCTCCGCCACGAGGCTACGGGGGG

AlaValIleValValPheAspAlaLysAlaProSerPheArgHisGluAlaTyrGlyGly

260 280 300

TACAAGGCGGCCGGCCCCACGCCGGAGGACTTCCCGGCAACTGCCCTCATCAAG

TyrLysAlaGlyArgAlaProThrProGluAspPheProArgGlnLeuAlaLeuIleLys

81

320 340 360

XbaI

GAGCTGGTGGACCTCCGGGCTGGCGCGCTCGAGGTCCCGGCTACGAGGCGGACGAC

GluLeuValAspLeuLeuGlyLeuAlaArgLeuGluValProGlyTyrGluAlaAspAsp

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FIGURE 1

TAQ DNA POLYMERASE SEQUENCE
2/6

380 400 420
GTCCTGGCCAGCCTGGCCAAGAAGGCGAAAAGGAGGGTACGAGGTCCGCATCCTCAC
ValLeuAlaSerLeuAlaLysLysAlaGluLysGluGlyTyrGluValArgIleLeuThr
121

440 460 480
GCCGACAAAGACCTTACCAAGCTCCTTCCGACCGCATCCACGTCTCCACCCCGAGGGG
AlaAspLysAspLeuTyrGlnLeuLeuSerAspArgIleHisValLeuHisProGluGly

500 520 540
Asp718
TACCTCATCACCCGGCCTGGCTTGGAAAAGTACGGCCTGAGGCCGACCAGTGGGCC
TyrLeuIleThrProAlaTrpLeuTrpGluLysTyrGlyLeuArgProAspGlnTrpAla
161

560 580 600
GAECTACCGGGCCCTGACCGGGGACGAGTCCGACAACCTCCCGGGGTCAAGGGCATCGGG
AspTyrArgAlaLeuThrGlyAspGluSerAspAsnLeuProGlyValLysGlyIleGly

620 640 660
HindIII
GAGAAGACGGCGAGGAAGCTCTGGAGGAGTGGGGGAGCCTGGAAGCCCTCCTCAAGAAC
GluLysThrAlaArgLysLeuLeuGluTrpGlySerLeuGluAlaLeuLysAsn
201

680 700 720
CTGGACCGGCTGAAGCCCGCCATCCGGAGAAGATCCTGGCCCACATGGACGATCTGAAG
LeuAspArgLeuLysProAlaIleArgGluLysIleLeuAlaHisMetAspAspLeuLys

740 760 780
CTCTCCTGGGACCTGGCCAAGGTGCGCACCGACCTGCCCTGGAGGTGGACTTCGCCAAA
LeuSerTrpAspLeuAlaLysValArgThrAspLeuProLeuGluValAspPheAlaLys
241

800 820 840
AGGCAGGGAGCCGACCGGGAGAGGCTTAGGGCCTTCTGGAGAGGCTTGAGTTGGCAGC
ArgArgGluProAspArgGluArgLeuArgAlaPheLeuGluArgLeuPheGlySer

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FIGURE 1

TAQ DNA POLYMERASE SEQUENCE
3/6

860

880
BstXI

900

CTCCTCCACGAGTTGGCCTCTGGAAAGCCCCAAGGCCCTGGAGGAGGCCCTGGCCC
LeuLeuHisGluPheGlyLeuLeuGluSerProLysAlaLeuGluGluAlaProTrpPro
281 290

920

940

960

CCGCCGGAAAGGGGCCTCGTGGCTTGTGCTTCGGCAAGGAGCCATGTGGGCCGAT
ProProGluGlyAlaPheValGlyPheValLeuSerArgLysGluProMetTrpAlaAsp

980

1000

1020

CTTCTGGCCCTGGCCGCCAGGGGGCCGGTCCACCAGGGCCCCCGAGCCTATAAA
LeuLeuAlaLeuAlaAlaAlaArgGlyGlyArgValHisArgAlaProGluProTyrLys
321

1040

1060

1080

GCCCTCAGGGACCTGAAGGAGGCCGGGGCTTCTCGCAAAGACCTGAGCGTTCTGGCC
AlaLeuArgAspLeuLysGluAlaArgGlyLeuLeuAlaLysAspLeuSerValLeuAla

1100

1120

1140

CTGAGGGAAAGGCCTGGCCTCCGCCGGCGACGACCCATGCTCCTCGCCTACCTCCTG
LeuArgGluGlyLeuGlyLeuProProGlyAspAspProMetLeuLeuAlaTyrLeuLeu
361

1160

1180

1200

GACCTTCCAACACCACCCCCCGAGGGGGTGGCCCGGCGTACGGCGGGGAGTGGACGGAG
AspProSerAsnThrThrProGluGlyValAlaArgArgTyrGlyGluTrpThrGlu

1220

1240

1260

GAGGGGGGGAGCGGGCCGCCCTTCCGAGAGGCTCTCGCCAACCTGTGGGGAGGCTT
GluAlaGlyGluArgAlaAlaLeuSerGluArgLeuPheAlaAsnLeuTrpGlyArgLeu
401

1280

1300

1320

GAGGGGGAGGAGAGGCTCCTTGGCTTACGGGAGGTGGAGAGGGCCCTTCCGCTGTC
GluGlyGluGluArgLeuLeuTrpLeuTyrArgGluValGluArgProLeuSerAlaVal

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FIGURE 1

TAQ DNA POLYMERASE SEQUENCE

4/6

1340

1360

1380

CTGGCCCACATGGAGGCCACGGGGTGCGCCTGGACGTGGCTATCTCAGGGCCTGTCC
LeuAlaHisMetGluAlaThrGlyValArgLeuAspValAlaTyrLeuArgAlaLeuSer
441

1400

1420

1440

XbaI

CTGGAGGTGGCCGAGGAGATCGCCCGCCTCGAGGCCGAGGTCTTCGCCCTGGCCGGCAC
LeuGluValAlaGluGluIleAlaArgLeuGluAlaGluValPheArgLeuAlaGlyHis

1460

1480

1500

PvuII

CCCTTCAACCTCAACTCCCGGACCAGCTGGAAAGGGTCCTTTGACGAGCTAGGGCTT
ProPheAsnLeuAsnSerArgAspGlnLeuGluArgValLeuPheAspGluLeuGlyLeu
481

1520

1540

1560

CCCGCCATCGGCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCCGTCTGGAG
ProAlaIleGlyLysThrGluLysThrGlyLysArgSerThrSerAlaAlaValLeuGlu

1580

1600

1620

PstI

SacI

GCCCTCCGCGAGGCCACCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAG
AlaLeuArgGluAlaHisProIleValGluLysIleLeuGlnTyrArgGluLeuThrLys
521

1640

1660

1680

CTGAAGAGCACCTACATTGACCCCTTGCCTGGACCTCATCCACCCAGGACGGGCCGCTC
LeuLysSerThrTyrIleAspProLeuProAspLeuIleHisProArgThrGlyArgLeu

1700

1720

1740

CACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAACGAGCTCCGATCCAAC
HisThrArgPheAsnGlnThrAlaThrAlaThrGlyArgLeuSerSerSerAspProAsn
561

1760

1780

1800

BamHI

CTCCAGAACATCCCCGTCCGCACCCGCTTGGGCAGAGGATCCGCCGGCCTTCATGCC
LeuGlnAsnIleProValArgThrProLeuGlyGlnArgIleArgArgAlaPheIleAla

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FIGURE 1

TAQ DNA POLYMERASE SEQUENCE
5/6

1820

5/6

1840

1860

SacI

GAGGAGGGTGGCTATTGGTGGCCCTGGACTATAGCCAGATAGAGCTCAGGGTGGCTGGCC
GluGluGlyTrpLeuLeuValAlaLeuAspTyrSerGlnIleGluLeuArgValLeuAla
601

1880

1900

1920

CACCTCTCCGGCGACGAGAACCTGATCCGGGTCTTCCAGGAGGGCGGGACATCCACACG
HisLeuSerGlyAspGluAsnLeuIleArgValPheGlnGluGlyArgAspIleHisThr

1940

1960

1980

PvuII

GAGACCGCCAGCTGGATGTTGGCGTCCCCCGGGAGGCCGTGGACCCCTGATGGCCGG
GluThrAlaSerTrpMetPheGlyValProArgGluAlaValAspProLeuMetArgArg
641

2000

2020

2040

GCGGCCAAGACCATCAACTTCGGGTCCCTACGGCATGTCGGCCCACCGCCTCTCCCAG
AlaAlaLysThrIleAsnPheGlyValLeuTyrGlyMetSerAlaHisArgLeuSerGln

2060

2080

2100

NheI

GAGCTAGCCATCCCTTACGAGGAGGCCAGGCCTTCATTGAGCGCTACTTCAGAGCTTC
GluLeuAlaIleProTyrGluGluAlaGlnAlaPheIleGluArgTyrPheGlnSerPhe
681

2120

2140

2160

CCCAAGGTGGGGCTGGATTGAGAAGACCTGGAGGAGGGCAGGAGGCCGGGTACGTG
ProLysValArgAlaTrpIleGluLysThrLeuGluGlyArgArgGlyTyrVal

2180

2200

2220

GAGACCCTTCGGCCGCCGCGCTACGTGCCAGACCTAGAGGCCGGGTGAAGAGCGTG
GluThrLeuPheGlyArgArgArgTyrValProAspLeuGluAlaArgValLysSerVal
721

FIGURE 1

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TAQ DNA POLYMERASE SEQUENCE
6/6

2240

2260

2280

CGGGAGGCGCCGAGCCATGGCCTCAACATGCCGTCCAGGCACCGCCGCCGACCTC
ArgGluAlaAlaGluArgMetAlaPheAsnMetProValGlnGlyThrAlaAlaAspLeu
741

2300

2320

2340

ATGAAGCTGGCTATGGTGAAGCTCTCCCCAGGCTGGAGGAAATGGGGCCAGGATGCTC
MetLysLeuAlaMetValLysLeuPheProArgLeuGluMetGlyAlaArgMetLeu

2360

2380

2400

XbaI

CTTCAGGTCCACGACGAGCTGGTCCCTGAGGCCAAAAGAGAGGGCGGAGGCCGTGGCC
LeuGlnValHisAspGluLeuValLeuGluAlaProLysGluArgAlaGluAlaValAla
781

2420

2440

2460

CGGCTGGCCAAGGAGGTATGGAGGGGTGTATCCCCTGGCCGTGCCCTGGAGGTGGAG
ArgLeuAlaLysGluValMetGluGlyValTyrProLeuAlaValProLeuGluValGlu

2480

2500

GTGGGGATAAGGGAGGACTGGCTCTCGCCAAGGAGTGATACCACC
ValGlyIleGlyGluAspTrpLeuSerAlaLysGluEnd
821 832

117387003

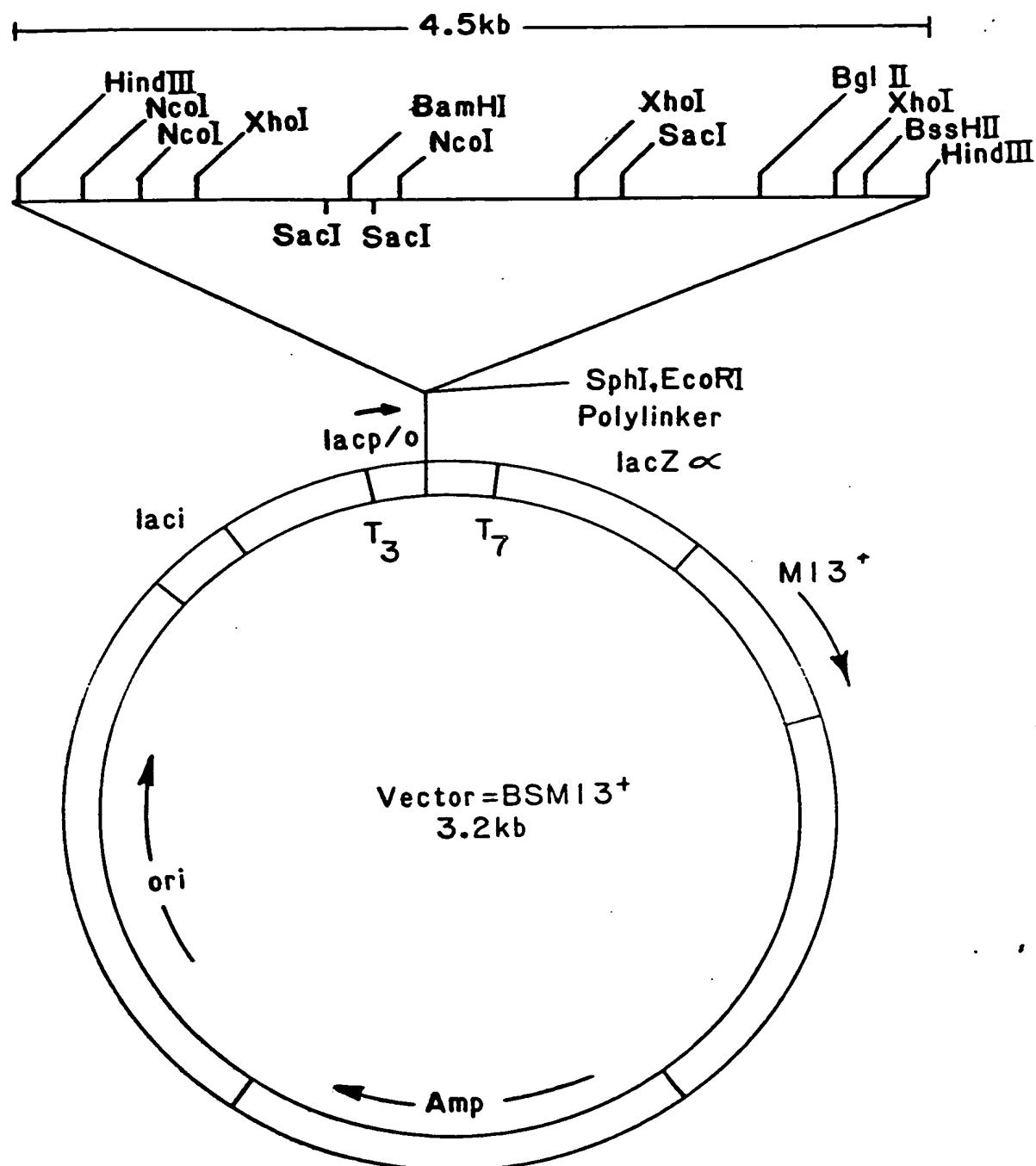


FIG. 2

11/387003

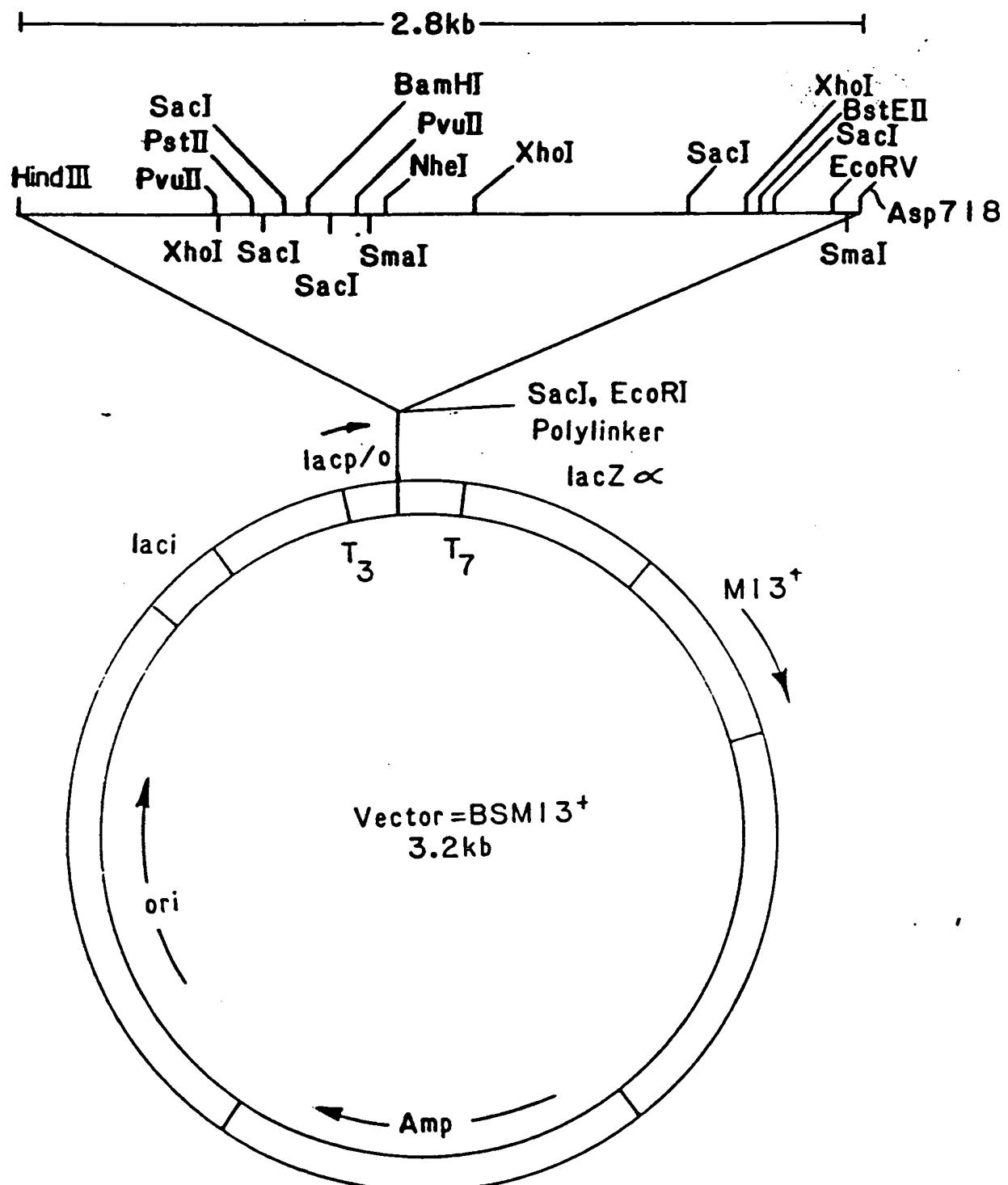


FIG. 3